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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/869,433

DATE: 06/12/2002
 TIME: 12:01:17

Input Set : A:\seqed.app.txt
 Output Set: N:\CRF3\06122002\I869433.raw

3 <110> APPLICANT: Aventis Pasteur Limited
 5 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof

7 <130> FILE REFERENCE: 77813-6
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/869,433
 C--> 10 <141> CURRENT FILING DATE: 2001-12-28

ENTERED

12 <150> PRIOR APPLICATION NUMBER: US 60/114,060
 13 <151> PRIOR FILING DATE: 1998-12-28
 15 <150> PRIOR APPLICATION NUMBER: US 60/123,967
 16 <151> PRIOR FILING DATE: 1999-03-12
 18 <150> PRIOR APPLICATION NUMBER: US 60/141,271
 19 <151> PRIOR FILING DATE: 1999-06-30

21 <160> NUMBER OF SEQ ID NOS: 4
 23 <170> SOFTWARE: PatentIn Ver. 2.0

27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1637

29 <212> TYPE: DNA

30 <213> ORGANISM: Chlamydia pneumoniae

32 <220> FEATURE:

33 <221> NAME/KEY: CDS

34 <222> LOCATION: (51)..(1595)

36 <400> SEQUENCE: 1

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38 Met Thr

39 1

41 aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg 104

42 Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro

43 5 10 15

45 ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc 152

46 Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe

47 20 25 30

49 ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act 200

50 Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr

51 35 40 45 50

53 ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc 248

54 Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile

55 55 60 65

57 aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat 296

58 Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr

59 70 75 80

61 gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg 344

62 Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val

63 85 90 95

65 gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat 392

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67 100 105 110
69 ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag 440
70 Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln
71 115 120 125 130
73 gcc atc cta cct cca gga ttg cta gga ctc gtt gcc atc tta aga aac 488
74 Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn
75 135 140 145
77 tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc 536
78 Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val
79 150 155 160
81 atg cta tct cta atg ttc tgg gga ttt gct aat gaa att aca aaa atc 584
82 Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile
83 165 170 175
85 cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att 632
86 His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile
87 180 185 190
89 tct tta cta gct tct ggt cgt gca att gtt tgg gct tca aag ttg aga 680
90 Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg
91 195 200 205 210
93 gct tcc gtt tct gaa ggt gta gat cct tgg gga att tct tta cgt ctt 728
94 Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu
95 215 220 225
97 ttg atg gct atg act att gta tct gga ctt gtt ctt atg gcc agt tac 776
98 Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr
99 230 235 240
101 tgg tgg atc aat aag aac gta ttg acc gat cct cgc ttc tat aat cca 824
102 Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro
103 245 250 255
105 gaa gaa atg caa aag ggg aaa aaa ggt gct aaa cct aaa atg aat atg 872
106 Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met
107 260 265 270
109 aaa gat agc ttc ctc tat ctt gat aga tct cct tat att ctt tta tta 920
110 Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu Leu Leu
111 275 280 285 290
113 act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg 968
114 Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val
115 295 300 305
117 act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat 1016
118 Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr
119 310 315 320
121 agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta 1064
122 Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val
123 325 330 335
126 ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg 1112
127 Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp
128 340 345 350
130 tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc 1160
131 Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile

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135 Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val
136          375          380          385
138 gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct 1256
139 Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala
140          390          395          400
142 ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca 1304
143 Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser
144          405          410          415
146 act aaa gaa atg gcc tat atc cct ctt gac caa gag caa aaa gtc aaa 1352
147 Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys
148          420          425          430
150 ggt aag gct gct att gat gta gtt gcc gcc cgc ttc gga aaa tca gga 1400
151 Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly
152 435          440          445          450
154 gga gct tta atc caa caa ggt ttg ctc gtt atc tgt gga agt att gga 1448
155 Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly
156          455          460          465
158 gct atg acc cct tat ctt gca gtg att ctt ctt ttc atc att gct att 1496
159 Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile
160          470          475          480
162 tgg ttg gtt tct gca act aag tta aac aaa cta ttc tta gcg cag tct 1544
163 Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser
164          485          490          495
166 gct ctt aaa gaa caa gaa gtg gct caa gaa gat tca gct cct gct tct 1592
167 Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser
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171 Ser
172 515
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 515
177 <212> TYPE: PRT
178 <213> ORGANISM: Chlamydia pneumoniae
180 <400> SEQUENCE: 2
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184 Trp Pro Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu
185 20 25 30
187 Met Phe Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys
188 35 40 45
190 Asp Thr Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro
191 50 55 60
193 Phe Ile Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu
194 65 70 75 80
196 Ile Tyr Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr
197 85 90 95
199 Ala Val Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val

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206		130					135					140				
208	Arg	Asn	Trp	Thr	Phe	Ala	Ala	Phe	Tyr	Val	Leu	Ala	Glu	Leu	Trp	Gly
209	145					150					155					160
211	Ser	Val	Met	Leu	Ser	Leu	Met	Phe	Trp	Gly	Phe	Ala	Asn	Glu	Ile	Thr
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214	Lys	Ile	His	Glu	Ala	Lys	Arg	Phe	Tyr	Ala	Leu	Phe	Gly	Ile	Gly	Ala
215				180					185					190		
217	Asn	Ile	Ser	Leu	Leu	Ala	Ser	Gly	Arg	Ala	Ile	Val	Trp	Ala	Ser	Lys
218			195					200					205			
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224	225					230					235					240
226	Ser	Tyr	Trp	Trp	Ile	Asn	Lys	Asn	Val	Leu	Thr	Asp	Pro	Arg	Phe	Tyr
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231	Asn	Met	Lys	Asp	Ser	Phe	Leu	Tyr	Leu	Asp	Arg	Ser	Pro	Tyr	Ile	Leu
232			275						280				285			
234	Leu	Leu	Thr	Leu	Leu	Val	Ile	Ala	Tyr	Gly	Ile	Cys	Ile	Asn	Leu	Ile
235		290					295					300				
237	Glu	Val	Thr	Trp	Lys	Ser	Gln	Leu	Lys	Leu	Gln	Tyr	Pro	Asn	Met	Asn
238	305					310					315					320
240	Asp	Tyr	Ser	Glu	Phe	Met	Gly	Asn	Phe	Ser	Phe	Trp	Thr	Gly	Val	Val
241					325					330					335	
243	Ser	Val	Leu	Ile	Met	Leu	Phe	Val	Gly	Gly	Asn	Val	Ile	Arg	Lys	Phe
244				340					345					350		
247	Gly	Trp	Leu	Thr	Gly	Ala	Leu	Val	Thr	Pro	Val	Met	Val	Leu	Leu	Thr
248			355					360					365			
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256	Gly	Ala	Ile	Gln	Asn	Ile	Leu	Ser	Lys	Ser	Thr	Lys	Tyr	Ala	Leu	Phe
257					405					410					415	
259	Asp	Ser	Thr	Lys	Glu	Met	Ala	Tyr	Ile	Pro	Leu	Asp	Gln	Glu	Gln	Lys
260																

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274 Gln Ser Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro
275 500 505 510
277 Ala Ser Ser
278 515
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 43
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: 5' PCR primer
289 <400> SEQUENCE: 3
290 ataagaatgc ggccgccacc atgacaaaaa ccgaagaaaa acc 43
293 <210> SEQ ID NO: 4
294 <211> LENGTH: 29
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: 3' PCR primer
301 <400> SEQUENCE: 4
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/869,433

DATE: 06/12/2002

TIME: 12:01:18

Input Set : A:\seqed.app.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date